

## SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Novel cytochrome P450 monooxygenases and their use for the oxidation of organic substrates

<130> M/40241

<140>

<141>

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 3150

<212> DNA

<213> Bacillus megaterium

<220>

<221> CDS

<222> (4)...(3150)

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Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys  
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aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa 96  
Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys  
20 25 30

att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt 144  
Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg  
35 40 45

gta acg cgc tac tta tca agt cag cgt cta att aaa gaa gca tgc gat 192  
Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp  
50 55 60

gaa tca cgc ttt gat aaa aac tta agt caa gcg ctt aaa ttt gta cgt 240  
Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg  
65 70 75

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## 26

gat ttt gca gga gac ggg tta ttt aca agc tgg acg cat gaa aaa aat	288
Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn	
80 85 90 95	
 tgg aaa aaa gcg cat aat atc tta ctt cca agc ttc agt cag cag gca	336
Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala	
100 105 110	
 atg aaa ggc tat cat gcg atg atg gtc gat atc gcc gtg cag ctt gtt	384
Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val	
115 120 125	
 caa aag tgg gag cgt cta aat gca gat gag cat att gaa gta ccg gaa	432
Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu	
130 135 140	
 gac atg aca cgt tta acg ctt gat aca att ggt ctt tgc ggc ttt aac	480
Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn	
145 150 155	
 tat cgc ttt aac agc ttt tac cga gat cag cct cat cca ttt att aca	528
Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr	
160 165 170 175	
 agt atg gtc cgt gca ctg gat gaa gca atg aac aag ctg cag cga gca	576
Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala	
180 185 190	
 aat cca gac gac cca gct tat gat gaa aac aag cgc cag ttt caa gaa	624
Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu	
195 200 205	
 gat atc aag gtg atg aac gac cta gta gat aaa att att gca gat cgc	672
Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg	
210 215 220	
 aaa gca agc ggt gaa caa agc gat gat tta tta acg cat atg cta aac	720
Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn	
225 230 235	
 gga aaa gat cca gaa acg ggt gag ccg ctt gat gac gag aac att cgc	768
Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg	
240 245 250 255	
 tat caa att att aca ttc tta att gcg gga cac gaa aca aca agt ggt	816
Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly	
260 265 270	
 ctt tta tca ttt gcg ctg tat ttc tta gtg aaa aat cca cat gta tta	864
Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu	
275 280 285	

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caa aaa gca gca gaa gaa gca gca cga gtt cta gta gat cct gtt cca		912
Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro		
290	295	300
agc tac aaa caa gtc aaa cag ctt aaa tat gtc ggc atg gtc tta aac		960
Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn		
305	310	315
gaa gcg ctg cgc tta tgg cca act gct cct gcg ttt tcc cta tat gca		1008
Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala		
320	325	330
aaa gaa gat acg gtg ctt gga gga gaa tat cct tta gaa aaa ggc gac		1056
Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp		
340	345	350
gaa cta atg gtt ctg att cct cag ctt cac cgt gat aaa aca att tgg		1104
Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp		
355	360	365
gga gac gat gtg gaa gag ttc cgt cca gag cgt ttt gaa aat cca agt		1152
Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser		
370	375	380
gcg att ccg cag cat gcg ttt aaa ccg ttt gga aac ggt cag cgt gcg		1200
Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala		
385	390	395
tgt atc ggt cag cag ttc gct ctt cat gaa gca acg ctg gta ctt ggt		1248
Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly		
400	405	410
415		
atg atg cta aaa cac ttt gac ttt gaa gat cat aca aac tac gag ctg		1296
Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu		
420	425	430
gat att aaa gaa act tta acg tta aaa cct gaa ggc ttt gtg gta aaa		1344
Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys		
435	440	445
gca aaa tcg aaa aaa att ccg ctt ggc ggt att cct tca cct agc act		1392
Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr		
450	455	460
gaa cag tct gct aaa aaa gta cgc aaa aag gca gaa aac gct cat aat		1440
Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn		
465	470	475
acg ccg ctg ctt gtg cta tac ggt tca aat atg gga aca gct gaa gga		1488
Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly		
480	485	490
495		

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## 28

acg gcg cgt gat tta gca gat att gca atg agc aaa gga ttt gca ccg 1536  
 Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro  
 500 505 510

cag gtc gca acg ctt gat tca cac gcc gga aat ctt ccg cgc gaa gga 1584  
 Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly  
 515 520 525

gct gta tta att gta acg gcg tct tat aac ggt cat ccg cct gat aac 1632  
 Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn  
 530 535 540

gca aag caa ttt gtc gac tgg tta gac caa gcg tct gct gat gaa gta 1680  
 Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val  
 545 550 555

aaa ggc gtt cgc tac tcc gta ttt gga tgc ggc gat aaa aac tgg gct 1728  
 Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala  
 560 565 570 575

act acg tat caa aaa gtg cct gct ttt atc gat gaa acg ctt gcc gct 1776  
 Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala  
 580 585 590

aaa ggg gca gaa aac atc gct gac cgc ggt gaa gca gat gca agc gac 1824  
 Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp  
 595 600 605

gac ttt gaa ggc aca tat gaa gaa tgg cgt gaa cat atg tgg agt gac 1872  
 Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp  
 610 615 620

gta gca gcc tac ttt aac ctc gac att gaa aac agt gaa gat aat aaa 1920  
 Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys  
 625 630 635

tct act ctt tca ctt caa ttt gtc gac agc gcc gcg gat atg ccg ctt 1968  
 Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu  
 640 645 650 655

gcg aaa atg cac ggt gcg ttt tca acg aac gtc gta gca agc aaa gaa 2016  
 Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu  
 660 665 670

ctt caa cag cca ggc agt gca cga agc acg cga cat ctt gaa att gaa 2064  
 Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu  
 675 680 685

ctt cca aaa gaa gct tct tat caa gaa gat cat tta ggt gtt att 2112  
 Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile  
 690 695 700

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10031246 011702

## 29

cct cgc aac tat gaa gga ata gta aac cgt gta aca gca agg ttc ggc 2160  
 Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly  
 705 710 715

cta gat gca tca cag caa atc cgt ctg gaa gca gaa gaa aaa tta 2208  
 Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu  
 720 725 730 735

gct cat ttg cca ctc gct aaa aca gta tcc gta gaa gag ctt ctg caa 2256  
 Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln  
 740 745 750

tac gtg gag ctt caa gat cct gtt acg cgc acg cag ctt cgc gca atg 2304  
 Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met  
 755 760 765

gct gct aaa acg gtc tgc ccg ccg cat aaa gta gag ctt gaa gcc ttg 2352  
 Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu  
 770 775 780

ctt gaa aag caa gcc tac aaa gaa caa gtg ctg gca aaa cgt tta aca 2400  
 Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr  
 785 790 795

atg ctt gaa ctg ctt gaa aaa tac ccg gcg tgt gaa atg aaa ttc agc 2448  
 Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser  
 800 805 810 815

gaa ttt atc gcc ctt ctg cca agc ata cgc ccg cgc tat tac tcg att 2496  
 Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile  
 820 825 830

tct tca tca cct cgt gtc gat gaa aaa caa gca agc atc acg gtc agc 2544  
 Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser  
 835 840 845

gtt gtc tca gga gaa gcg tgg agc gga tat gga gaa tat aaa gga att 2592  
 Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile  
 850 855 860

gcg tcg aac tat ctt gcc gag ctg caa gaa gga gat acg att acg tgc 2640  
 Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys  
 865 870 875

ttt att tcc aca ccg cag tca gaa ttt acg ctg cca aaa gac cct gaa 2688  
 Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu  
 880 885 890 895

acg ccg ctt atc atg gtc gga ccg gga aca ggc gtc gcg ccg ttt aga 2736  
 Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg  
 900 905 910

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## 30

ggc ttt gtg cag gcg cgc aaa cag cta aaa gaa caa gga cag tca ctt 2784  
 Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu  
 915 920 925

gga gaa gca cat tta tac ttc ggc tgc cgt tca cct cat gaa gac tat 2832  
 Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr  
 930 935 940

ctg tat caa gaa gag ctt gaa aac gcc caa agc gaa ggc atc att acg 2880  
 Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr  
 945 950 955

ctt cat acc gct ttt tct cgc atg cca aat cag ccg aaa aca tac gtt 2928  
 Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val  
 960 965 970 975

cag cac gta atg gaa caa gac ggc aag aaa ttg att gaa ctt ctt gat 2976  
 Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp  
 980 985 990

caa gga gcg cac ttc tat att tgc gga gac gga agc caa atg gca cct 3024  
 Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro  
 995 1000 1005

gcc gtt gaa gca acg ctt atg aaa agc tat gct gac gtt cac caa gtg 3072  
 Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val  
 1010 1015 1020

agt gaa gca gac gct cgc tta tgg ctg cag cag cta gaa gaa aaa ggc 3120  
 Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly  
 1025 1030 1035

cga tac gca aaa gac gtg tgg gct ggg taa 3150  
 Arg Tyr Ala Lys Asp Val Trp Ala Gly  
 1040 1045

<210> 2

<211> 1048

<212> PRT

<213> *Bacillus megaterium*

<400> 2

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn  
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Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile  
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Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val  
 35 40 45

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## 31

Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu  
 50 55 60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp  
 65 70 75 80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp  
 85 90 95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met  
 100 105 110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln  
 115 120 125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp  
 130 135 140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr  
 145 150 155 160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser  
 165 170 175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn  
 180 185 190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp  
 195 200 205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys  
 210 215 220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly  
 225 230 235 240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr  
 245 250 255

Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu  
 260 265 270

Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln  
 275 280 285

Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser  
 290 295 300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu  
 305 310 315 320

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Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys  
 325 330 335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu  
 340 345 350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly  
 355 360 365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala  
 370 375 380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys  
 385 390 395 400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met  
 405 410 415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp  
 420 425 430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala  
 435 440 445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu  
 450 455 460

Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr  
 465 470 475 480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr  
 485 490 495

Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln  
 500 505 510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala  
 515 520 525

Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala  
 530 535 540

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys  
 545 550 555 560

Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr  
 565 570 575

Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys  
 580 585 590

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Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp  
 595 600 605

Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val  
 610 615 620

Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser  
 625 630 635 640

Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala  
 645 650 655

Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu  
 660 665 670

Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu  
 675 680 685

Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro  
 690 695 700

Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu  
 705 710 715 720

Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Lys Leu Ala  
 725 730 735

His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr  
 740 745 750

Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala  
 755 760 765

Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu  
 770 775 780

Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met  
 785 790 795 800

Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu  
 805 810 815

Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser  
 820 825 830

Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val  
 835 840 845

Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala  
 850 855 860

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Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe  
 865 870 875 880

Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr  
 885 890 895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly  
 900 905 910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly  
 915 920 925

Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu  
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu  
 945 950 955 960

His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln  
 965 970 975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln  
 980 985 990

Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala  
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser  
 1010 1015 1020

Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg  
 1025 1030 1035 1040

Tyr Ala Lys Asp Val Trp Ala Gly  
 1045

<210> 3

<211> 30

<212> DNA

<213> Synthetic sequence

<220>

<223> Description of the synthetic sequence: PCR primer

<400> 3

gcaggagacg ggttgnnnac aagctggacg

30

<210> 4

<211> 30

<212> DNA

<213> Synthetic sequence

&lt;220&gt;

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 4

cgtccagtt gtnnncaacc cgtctcctgc

30

&lt;210&gt; 5

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Synthetic sequence

&lt;220&gt;

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 5

gaagcaatga acaagnnnca gcgagcaaat ccag

34

&lt;210&gt; 6

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Synthetic sequence

&lt;220&gt;

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 6

ctggatttgc tcgctgnnnnc ttgttcattg

30

&lt;210&gt; 7

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Synthetic sequence

&lt;220&gt;

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 7

gctttgataa aaacttaaag tcaannnctt aaatttgtac g

41

&lt;210&gt; 8

&lt;211&gt; 40

&lt;212&gt; DNA

&lt;213&gt; Synthetic sequence

&lt;220&gt;

&lt;223&gt; Description of the synthetic sequence: PCR primer

&lt;400&gt; 8

cgtacaaatt taagnnnntg acttaagttt ttatcaaagc

40

&lt;210&gt; 9

&lt;211&gt; 1049

&lt;212&gt; PRT

&lt;213&gt; Bacillus megaterium

&lt;400&gt; 9

Met Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys  
1 5 10 15

Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys  
20 25 30

Ile Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg  
35 40 45

Val Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp  
50 55 60

Glu Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg  
65 70 75 80

Asp Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn  
85 90 95

Trp Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala  
100 105 110

Met Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val  
115 120 125

Gln Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu  
130 135 140

Asp Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn  
145 150 155 160

Tyr Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr  
165 170 175

Ser Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala  
180 185 190

Asn Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu  
195 200 205

Asp Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg  
210 215 220

Lys Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn  
225 230 235 240

37

Gly Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg  
245 250 255

Tyr Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly  
260 265 270

Leu Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu  
275 280 285

Gln Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro  
290 295 300

Ser Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn  
305 310 315 320

Glu Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala  
325 330 335

Lys Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp  
340 345 350

Glu Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp  
355 360 365

Gly Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser  
370 375 380

Ala Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala  
385 390 395 400

Cys Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly  
405 410 415

Met Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu  
420 425 430

Asp Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys  
435 440 445

Ala Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr  
450 455 460

Glu Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn  
465 470 475 480

Thr Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly  
485 490 495

Thr Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro  
500 505 510

## 38

Gln Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly  
515 520 525

Ala Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn  
530 535 540

Ala Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val  
545 550 555 560

Lys Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala  
565 570 575

Thr Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala  
580 585 590

Lys Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp  
595 600 605

Asp Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp  
610 615 620

Val Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys  
625 630 635 640

Ser Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu  
645 650 655

Ala Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu  
660 665 670

Leu Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu  
675 680 685

Leu Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile  
690 695 700

Pro Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly  
705 710 715 720

Leu Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Lys Leu  
725 730 735

Ala His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln  
740 745 750

Tyr Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met  
755 760 765

Ala Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu  
770 775 780

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Leu Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr  
785 790 795 800

Met Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser  
805 810 815

Glu Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile  
820 825 830

Ser Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser  
835 840 845

Val Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile  
850 855 860

Ala Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys  
865 870 875 880

Phe Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu  
885 890 895

Thr Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg  
900 905 910

Gly Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu  
915 920 925

Gly Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr  
930 935 940

Leu Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr  
945 950 955 960

Leu His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val  
965 970 975

Gln His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp  
980 985 990

Gln Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro  
995 1000 1005

Ala Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val  
1010 1015 1020

Ser Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly  
1025 1030 1035 1040

Arg Tyr Ala Lys Asp Val Trp Ala Gly  
1045